

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/725,418
Source: IFWO
Date Processed by STIC: 10/18/04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/725,418

TIME: 10:47:48

Input Set : A:\78031566.app

Output Set: N:\CRF4\10182004\J725418.raw

3 <110> APPLICANT: ZOLLER, MARK
 4 LI, XIAODONG
 5 STASZEWSKI, LENA
 6 O'CONNELL, SHAWN
 7 ZOZULYA, SERGEY
 8 ADLER, JON
 9 XU, HONG
 10 ECHEVERRI, FERNANDO
 12 <120> TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
 13 THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
 14 IDENTIFICATION OF TASTE COMPOUNDS
 16 <130> FILE REFERENCE: 078003-0291566
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/725,418
 C--> 19 <141> CURRENT FILING DATE: 2003-12-03
 21 <150> PRIOR APPLICATION NUMBER: 60/300,434
 22 <151> PRIOR FILING DATE: 2001-06-26
 24 <150> PRIOR APPLICATION NUMBER: 60/304,749
 25 <151> PRIOR FILING DATE: 2001-07-13
 27 <150> PRIOR APPLICATION NUMBER: 60/310,493
 28 <151> PRIOR FILING DATE: 2001-08-08
 30 <150> PRIOR APPLICATION NUMBER: 60/331,771
 31 <151> PRIOR FILING DATE: 2001-11-21
 33 <150> PRIOR APPLICATION NUMBER: 60/339,472
 34 <151> PRIOR FILING DATE: 2001-12-14
 36 <150> PRIOR APPLICATION NUMBER: 60/372,090
 37 <151> PRIOR FILING DATE: 2002-04-15
 39 <150> PRIOR APPLICATION NUMBER: 60/374,143
 40 <151> PRIOR FILING DATE: 2002-04-22
 42 <160> NUMBER OF SEQ ID NOS: 19
 44 <170> SOFTWARE: PatentIn Ver. 2.1
 46 <210> SEQ ID NO: 1
 47 <211> LENGTH: 5
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Description of Artificial Sequence: PDZIP sequence
 54 <400> SEQUENCE: 1
 55 Ser Val Ser Thr Trp
 56 1 5
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 14
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Artificial Sequence

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64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
66     sequence
68 <220> FEATURE:
69 <221> NAME/KEY: MOD_RES
70 <222> LOCATION: (1)
71 <223> OTHER INFORMATION: Thr or Arg
73 <220> FEATURE:
74 <221> NAME/KEY: MOD_RES
75 <222> LOCATION: (3)
76 <223> OTHER INFORMATION: Phe or Leu
78 <220> FEATURE:
79 <221> NAME/KEY: MOD_RES
80 <222> LOCATION: (4)
81 <223> OTHER INFORMATION: Arg, Gln or Pro
83 <220> FEATURE:
84 <221> NAME/KEY: MOD_RES
85 <222> LOCATION: (6)
86 <223> OTHER INFORMATION: Arg or Thr
88 <220> FEATURE:
89 <221> NAME/KEY: MOD_RES
90 <222> LOCATION: (7)
91 <223> OTHER INFORMATION: Ser, Pro or Val
93 <220> FEATURE:
94 <221> NAME/KEY: MOD_RES
95 <222> LOCATION: (8)
96 <223> OTHER INFORMATION: Val, Glu, Arg, Lys or Thr
98 <220> FEATURE:
99 <221> NAME/KEY: MOD_RES
100 <222> LOCATION: (11)
101 <223> OTHER INFORMATION: Ala or Glu
103 <220> FEATURE:
104 <221> NAME/KEY: MOD_RES
105 <222> LOCATION: (12)
106 <223> OTHER INFORMATION: Trp or Leu
108 <220> FEATURE:
109 <221> NAME/KEY: MOD_RES
110 <222> LOCATION: (13)
111 <223> OTHER INFORMATION: Arg, His or Gly
113 <400> SEQUENCE: 2
W--> 114 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
115     1           5           10
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 15
120 <212> TYPE: PRT
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
125     sequence

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127 <220> FEATURE:
128 <221> NAME/KEY: MOD_RES
129 <222> LOCATION: (1)
130 <223> OTHER INFORMATION: Leu or Gln
132 <220> FEATURE:
133 <221> NAME/KEY: MOD_RES
134 <222> LOCATION: (3)
135 <223> OTHER INFORMATION: Glu, Gly or Thr
137 <220> FEATURE:
138 <221> NAME/KEY: MOD_RES
139 <222> LOCATION: (4)
140 <223> OTHER INFORMATION: Asn, Arg or Cys
142 <220> FEATURE:
143 <221> NAME/KEY: MOD_RES
144 <222> LOCATION: (7)
145 <223> OTHER INFORMATION: Arg or Glu
147 <220> FEATURE:
148 <221> NAME/KEY: MOD_RES
149 <222> LOCATION: (9)
150 <223> OTHER INFORMATION: Arg or Lys
152 <220> FEATURE:
153 <221> NAME/KEY: MOD_RES
154 <222> LOCATION: (10)
155 <223> OTHER INFORMATION: Cys, Gly or Phe
157 <220> FEATURE:
158 <221> NAME/KEY: MOD_RES
159 <222> LOCATION: (11)
160 <223> OTHER INFORMATION: Val, Leu or Ile
162 <220> FEATURE:
163 <221> NAME/KEY: MOD_RES
164 <222> LOCATION: (13)
165 <223> OTHER INFORMATION: Phe or Leu
167 <220> FEATURE:
168 <221> NAME/KEY: MOD_RES
169 <222> LOCATION: (14)
170 <223> OTHER INFORMATION: Ala or Ser
172 <220> FEATURE:
173 <221> NAME/KEY: MOD_RES
174 <222> LOCATION: (15)
175 <223> OTHER INFORMATION: Met or Leu
177 <400> SEQUENCE: 3
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      179 1 5 10 15
182 <210> SEQ ID NO: 4
183 <211> LENGTH: 858
184 <212> TYPE: PRT
185 <213> ORGANISM: Rattus sp.
187 <400> SEQUENCE: 4
188 Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu

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189	1				5					10					15	
191	Leu	Gly	Met	Gly	Ser	Ser	Leu	Cys	Leu	Ser	Gln	Gln	Phe	Lys	Ala	Gln
192				20					25					30		
194	Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Thr	Thr	Glu	Glu
195			35					40					45			
197	Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Gly	Ile	Leu	Cys	Thr	Arg
198		50					55					60				
200	Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val
201	65					70				75					80	
203	Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly
204				85					90					95		
206	Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Pro
207			100					105					110			
209	Ser	Leu	Met	Phe	Met	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr
210			115					120					125			
212	Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro
213		130				135					140					
215	His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe
216	145				150					155						160
218	Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp
219				165					170					175		
221	Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val
222			180					185					190			
224	Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp
225			195				200					205				
227	Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser
228		210				215					220					
230	Ile	Phe	Ser	Gly	Leu	Ala	Asn	Ser	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu
231	225				230					235						240
233	Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val
234				245					250				255			
236	Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val
237			260					265					270			
239	Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile
240			275				280					285				
242	Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu
243		290				295					300					
245	Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr
246	305				310					315					320	
248	Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His
249				325				330					335			</

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263 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
264                               405                               410                               415
266 Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
267                               420                               425                               430
269 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
270                               435                               440                               445
272 Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
273                               450                               455                               460
275 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
276 465                               470                               475                               480
278 Phe Asn Gly Thr Leu Gln Leu Gln His Ser Lys Met Tyr Trp Pro Gly
279                               485                               490                               495
281 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
282                               500                               505                               510
284 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
285                               515                               520                               525
287 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
288                               530                               535                               540
290 Pro Cys Gly Lys Asp Gln Trp Ser Pro Glu Lys Ser Thr Thr Cys Leu
291 545                               550                               555                               560
293 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
294                               565                               570                               575
296 Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
297                               580                               585                               590
299 Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
300                               595                               600                               605
302 Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
303                               610                               615                               620
305 Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
306 625                               630                               635                               640
308 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
309                               645                               650                               655
311 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
312                               660                               665                               670
314 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
315                               675                               680                               685
317 Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
318                               690                               695                               700
320 Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
321 705                               710                               715                               720
323 Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
324                               725                               730                               735
326 Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
327                               740                               745                               750
329 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
330                               755                               760                               765
332 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
333                               770                               775                               780
335 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/725,418

DATE: 10/18/2004
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Input Set : A:\78031566.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,3,4,6,7,8,11,12,13

Seq#:3; Xaa Pos. 1,3,4,7,9,10,11,13,14,15

Seq#:13; Xaa Pos. 120,121

Seq#:15; Xaa Pos. 8,15,59,62,76,117,128,136,168,173,175,176,203,226

VERIFICATION SUMMARY

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Input Set : A:\78031566.app

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L:18 M:270 C: Current Application Number differs, Replaced Current Application Number
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:112
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15